Changed the margins in cases where the sequence text was averaged down to the next line.  Edited a format error in the Current Application Data section, specifically:  Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other different the mandatory heading and subheadings for "Current Application Data".  Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integrated the spelling of a mandatory field (the headings or subheadings), specifically:  Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:		Changed a file from non-ASCII to ASCII  Changed a file from non-ASCII to ASCII
Edited a format error in the Current Application Data section, specifically:  Edited the Current Application Data section with the actual current number. The number inputted by the applicant was a the prior application data; or other supplication Data. Added the mandatory heading and subheadings for "Current Application Data".  Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integration of a mandatory field (the headings or subheadings), specifically:  Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: one-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end page numbers throughout text; other invalid text, such as inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited ideptifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		
Edited the Current Application Data section with the actual current number. The number inputted by tapplicant was the prior application data; or other  Added the mandatory heading and subheadings for "Current Application Data".  Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integrated the spelling of a mandatory field (the headings or subheadings), specifically:  Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		
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Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer Changed the spelling of a mandatory field (the headings or subheadings), specifically:  Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of page numbers throughout text; other invalid text, such as  Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited ideptifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other
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Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: non-ASCII *garbage* at the beginning/end of files; secretary initials/filename at end of page numbers throughout text; other invalid text, such as  Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer
Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: Inserted mandatory headings, specifically:  Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Changed the spelling of a mandatory field (the headings or subheadings), specifically:
Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: Inon-ASCII "garbage" at the beginning/end of files; Inserted secretary initials/filename at ending page numbers throughout text; Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
applicant placed a response below the subheading, this was moved to its appropriate place.  Inserted colons after headings/subheadings. Headings edited included:  FEB  Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: Inon-ASCII "garbage" at the beginning/end of files; Inserted secretary initials/filename at ending page numbers throughout text; Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
Deleted extra, invalid, headings used by an applicant, specifically:  Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically:  Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		applicant placed a reasonable below the cubbonding this was moved to its convenient place.
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Corrected an obvious error in the response, specifically:  Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:	•	Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of page numbers throughout text; other invalid text, such as
Edited identifiers where upper case is used but lower case is required, or vice versa.  Corrected an error in the Number of Sequences field, specifically:		Inserted mandatory headings, specifically:
Corrected an error in the Number of Sequences field, specifically:		Corrected an obvious error in the response, specifically:
		Edited identifiers where upper case is used but lower case is required, or vice versa.
A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted		Corrected an error in the Number of Sequences field, specifically:
·	•	A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted
Deleted <i>ending</i> stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (endue to a Patentin bug). Sequences corrected:		eleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (erro
Other:		
•	1	ue to a Patentin bug). Sequences corrected:
	1	ue to a Patentin bug). Sequences corrected:

## RECEIVED

## FEB 2 2 2002 TECH CENTER 1600/2900



1645

RAW SEQUENCE LISTING DATE: 02/19/2002 PATENT APPLICATION: US/09/765,231A TIME: 17:12:09

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    306 gtcaacagag caaggagaaa aaaggcagtc ctggaatcac attcttagca cacctacacc 1560
    308 tottgaaaat agaacaactt qoaqaattga qaqtqattoo tttootaaaa qtgtaaqaaa 1620
    310 gcatagagat ttgttcgtat ttagaatggg atcacgagga aaagagaagg aaagtgattt 1680
    312 ttttccacaa gatctgtaat gttatttcca cttataaagg aaataaaaaa tgaaaaacat 1740
    314 tatttggata tcaaaagcaa ataaaaaccc aattcagtct cttctaagca aaattqctaa 1800
    316 agagagatga accacattat aaagtaatct ttggctgtaa ggcattttca tctttccttc 1860
    318 gggttggcaa aatattttaa aggtaaaaca tgctggtgaa ccaggggtgt tgatggtgat 1920
    320 aagggaggaa tatagaatga aagactgaat cttcctttgt tgcacaaata gagtttggaa 1980
    322 aaagcctgtg aaaggtgtct tctttgactt aatgtcttta aaagtatcca gagatactac 2040
    324 aatattaaca taagaaaaga ttatatatta tttctqaatc qaqatqtcca taqtcaaatt 2100
    326 tgtaaatctt attcttttgt aatatttatt tatatttatt tatgacagtg aacattctga 2160
    328 ttttacatgt aaaacaagaa aagttgaaga agatatgtga agaaaaatgt atttttccta 2220
    333 <210> SEQ ID NO: 7
    334 <211> LENGTH: 712
    335 <212> TYPE: DNA
    336 <213> ORGANISM: Homo sapiens
    338 <400> SEQUENCE: 7
    340 cttaaaccta tttagtaatg ttttcccaag tttattttt atttttaatt ttttccccaa
    342 gtttattttt ctatttttt ttcatggaaa aatggggtaa cttagcagtt tcaatattga
                                                                         120
    344 agactgaagt ttaaaaaaaa tttaaattca aggtactttt aaaattcagt tagaaaagta
                                                                         180
    346 ggctttaaaa attattagag acaagagtac caaagcggtg tgtgtatgtg tgtgtgta
                                                                         240
    348 tgcatgcttg tggattggaa aaactttgga qactgattac ttttcattat atatqtqtca
    350 cagtgaaaca gcttttatgt gtcatgtaag attattgctt gcctctctaa ggaaggtcgt
                                                                         360
    352 gactgtttaa atagacgggc aaggtggaac cttttgaaag atgagctttt gaatataagt
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```

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02192002\1765231A.raw

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354 tgtctgctag atcatggttt gtattgaact aacaaggttt gcagatctgc tgacttatat
     356 aaagettttt gatteetaet aagetttaag atttaaaaaa tgtteaatgt tgaaatttet
     358 gtggggctct attittgctt tggctttctg gtgagagagt gaggaagcat tctttccttc
                                                                           600
     360 actaagttig tettietigt ettetggata gattgattit aagagaetaa gggaatttae
                                                                           660
     362 aaactaaaga ttttagtcat ctggtggaaa aggagacttt aagattgttt ag
                                                                           712
     365 <210> SEQ ID NO: 8
     366 <211> LENGTH: 1474
     367 <212> TYPE: DNA
     368 <213> ORGANISM: Homo sapiens
     370 <400> SEQUENCE: 8
     372 ctcagtggat aaaagaccta gagaatgtgt atcccagaag aagctggcca aggatatggg
     374 agcaaccacc atgggaccag aagtetetet ggggcaggtg tagtggtett getgettete
                                                                           120
     376 cagggaggga tctgcctaca aactggtttg ctactttacc aactgggtcc caggaccggc
                                                                           180
     240
     380 tattcattqc qccaqcatcq aaaacaacaa qqttatcatc aaqqacaaqa qtqaaqtqat
     382 gctctaccag accatcaaca gttctcaaaa ccaagaatcc caaactgaaa attctcttgt
                                                                           360
     384 ccattggagg gtacctgttt ggttccaaag ggttccaccc tatggtggat tcttctacat
                                                                           420
     386 cacgettgga atteattaae tecataatee tgtttetgag gaaccataae tttgatggae
                                                                           480
     388 tggatgtaag ctggatctac ccagatcaga aagaaaacac tcatttcact gtgctgattc
                                                                           540
     390 atgagttage agaageettt cagaaggact teacaaaate caccaaggaa aggettetet
                                                                           600
     392 tgactgcqqq qqqtatctqc aqqqaqqcaa atqattgata acaqctatca agttgaqaaa
                                                                           660
     394 ctggcaaaag atctggattt catcaacete ctgteetttg acttecatgg gtettgggaa
                                                                           720
     396 aageceetta teaetggeea caacageeet getgageaag gggtggeagg acagagggee
                                                                           780
     398 aageteetae tacaatgtgg aatatgetgt ggggtaetgg atacataagg gaatgeeate
                                                                           840
     400 agagaaggtg gtcatgggca tccccacata tggggcactc cttcacactg gcctctgcag
                                                                           900
     402 aaaccaccgt gggggcccct gcctctggcc ctggagctgc tggacccatc acagagtctt
     404 caggetteet ggeetattat gagatetgee agtteetgaa aggageeaag ateaegegge 1020
     406 tocaggatca graggittoco targeagica aggggaarca gigggitggg taigaigaig 1080
     408 tgaagagtat ggagaccaag gttcagttct taaagaattt aaacctggga ggagccatga 1140
     410 tetagtetat taacatagat aactteacta acaateeta caaccaagage cettaceete 1200
     412 ttqtccaaqc aqtcaaqaqa aqccttqqct ccctqtqaaq qattaactta caqaqaaqca 1260
    414 ggcaagatga cettgetgee tggggeetge teteteceag gaatteteat gtgggattee 1320
    416 ccttgccagg ccggcctttg gatctctctt ccaagccttt cctgacttcc tcttagatca 1380
     418 tagattggac ctggttttgt tttcctgcag ctgttgactt gttgccctga agtacaataa 1440
     420 aaaaaattca ttttqctcca qtaaaaaaaa aaaa
    423 <210> SEQ ID NO: 9
     424 <211> LENGTH: 592
     425 <212> TYPE: DNA
     426 <213> ORGANISM: Homo sapiens
W--> 427 <220> FEATURE:
W--> 428 <221> NAME/KEY: 1-592
     429 <222> LOCATION: unknown
     431 <223> OTHER INFORMATION: unsure at all n locations
W--> 432 <400> SEQUENCE: 9
     434 acttteetgg tgaegetttg ettttettet getettggtg agaaagtgee teettettee
W--> 436 caggatcagg acctctgcca tccagcgcca caaagagaca tttctgcaca cacactnnnn
                                                                           120
W--> 438 nnnnnnnnn nnnnnnnnn nnnnnnnnn nnccagagac aaacttaagg tgaggagaaa
                                                                           180
     440 gagcgctagt ttcacttgat ctccagcttc caacttaagc agaacttgag agcatccgaa
     442 ctcctggatt tcaggacaag tgaagaagat tctttgggct ataaagatga agagtctact
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY PATENT APPLICATION: US/09/765,231A DATE: 02/19/2002 TIME: 17:12:10

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02192002\1765231A.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:249 M:283 W: Missing Blank Line separator, <220> field identifier L:250 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6 L:254 M:283 W: Missing Blank Line separator, <400> field identifier L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:427 M:283 W: Missing Blank Line separator, <220> field identifier L:428 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9 L:432 M:283 W: Missing Blank Line separator, <400> field identifier  $L\!:\!436~M\!:\!341~W\!:$  (46) "n" or "Xaa" used, for SEQ ID#:9 L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:712 M:283 W: Missing Blank Line separator, <220> field identifier L:713 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14 L:717 M:283 W: Missing Blank Line separator, <400> field identifier L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 L:1146 M:283 W: Missing Blank Line separator, <220> field identifier L:1147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21 L:1151 M:283 W: Missing Blank Line separator, <400> field identifier L:1153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 L:1442 M:283 W: Missing Blank Line separator, <220> field identifier L:1443 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27 L:1447 M:283 W: Missing Blank Line separator, <400> field identifier L:1473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 L:1648 M:283 W: Missing Blank Line separator, <220> field identifier L:1649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30 L:1653 M:283 W: Missing Blank Line separator, <400> field identifier L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 L:2402 M:283 W: Missing Blank Line separator, <220> field identifier L:2403 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41 L:2407 M:283 W: Missing Blank Line separator, <400> field identifier L:2445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 L:2512 M:283 W: Missing Blank Line separator, <220> field identifier L:2513 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42 L:2517 M:283 W: Missing Blank Line separator, <400> field identifier L:2519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 L:3102 M:283 W: Missing Blank Line separator, <220> field identifier L:3103 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:61 L:3107 M:283 W: Missing Blank Line separator, <400> field identifier L:3109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 L:3111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 L:3436 M:283 W: Missing Blank Line separator, <220> field identifier L:3437 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:79 L:3441 M:283 W: Missing Blank Line separator, <400> field identifier L:3445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 L:3447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 L:3465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 L:3474 M:283 W: Missing Blank Line separator, <220> field identifier L:3475 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80 VERIFICATION SUMMARYDATE: 02/19/2002PATENT APPLICATION: US/09/765,231ATIME: 17:12:10

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02192002\1765231A.raw

L:3479 M:283 W: Missing Blank Line separator, <400> field identifier

L:3481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 L:3483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80